

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Quartermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.
- (ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
CELL LOCUS-1
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-034
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864/9741
(C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
 20 25 30
 Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
 35 40 45
 Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
 50 55 60
 Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
 65 70 75 80
 Leu Pro Leu Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
 20 25 30
 Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 35 40 45
 Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
 50 55 60
 Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
 65 70 75 80
 Leu Pro Val Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
 20 25 30
 His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
 35 40 45
 Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
 50 55 60
 Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
 65 70 75 80
 Ile Pro Lys Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
 20 25 30
 Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
 35 40 45
 Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
 50 55 60
 Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1 5 10 15
Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
20 25 30
Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45
Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
50 55 60
Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65 70 75 80
Arg Pro Val Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1 5 10 15
Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
20 25 30
Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
35 40 45
Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60
Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65 70 75 80
Ile Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1 5 10 15
Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
20 25 30
Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
35 40 45
Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
50 55 60
Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65 70 75 80
His Pro Leu Thr Xaa
85

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Leu Xaa Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15
Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
20 25 30
Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
50 55 60
Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65 70 75 80
Xaa Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAAGTG ATATTTGATT TCCATTCTCA	60
TTCCCAGTGG CCTTGATATT TAAACTGATT CCTGCCACCA GGTCTTGGG CCACCCTGTC	120
CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCCTCC TGGCCTCAGG	180
CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCC GCATCCGCCG	240
CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGCCTGCGCG CACGGAAATC	300
GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC	360
AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG	420
TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTC	480
AGAAGCGCTG CGGGAGGAAA GACGTCTCTT TGATCTCTGA CAGGGCGGGG TTTACTGCTG	540
TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCCAGGACCA GCCCAGGTCA	600
CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT	651
Met Lys His Leu Val Ala Ala Trp Leu Leu Val	
1 5 10	
GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC	699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn	
15 20 25	
CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT	747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp	
30 35 40	
GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC	795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys	
45 50 55	
TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA	843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala	
60 65 70 75	
GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA	891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
80 85 90	
AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT	939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys	
95 100 105	
CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT	987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys	
110 115 120	
GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT	1035

Glu	Ala	Glu	Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	
125						130					135					
AAC	TAC	TCT	TGT	GAA	TGC	CCA	GGA	GAA	TTT	ATG	GGA	CGA	AAT	TGT	CAA	1083
Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	
140					145					150					155	
TAT	AAA	TGC	TCT	GGG	CAC	TTG	GGA	ATC	GAA	GGT	GGG	ATC	ATA	TCT	AAT	1131
Tyr	Lys	Cys	Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	
				160					165					170		
CAG	CAA	ATC	ACA	GCT	TCA	TCT	AAT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAG	1179
Gln	Gln	Ile	Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	
			175					180					185			
AAG	TGG	TAT	CCC	TAC	TAT	GCT	CGA	CTT	AAT	AAG	AAG	GGC	CTT	ATA	AAT	1227
Lys	Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	
		190					195					200				
GCC	TGG	ACA	GCT	GCT	GAA	AAT	GAC	AGA	TGG	CCA	TGG	ATT	CAG	ATA	AAT	1275
Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn	
	205					210					215					
TTG	CAA	AGA	AAA	ATG	AGA	GTC	ACT	GGT	GTT	ATT	ACC	CAA	GGA	GCA	AAA	1323
Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	
220					225					230					235	
AGG	ATT	GGA	AGC	CCA	GAG	TAC	ATA	AAA	TCC	TAC	AAA	ATT	GCC	TAC	AGC	1371
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser	
				240					245					250		
AAT	GAC	GGG	AAG	ACC	TGG	GCA	ATG	TAC	AAA	GTA	AAA	GGC	ACC	AAT	GAA	1419
Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	
			255					260					265			
GAG	ATG	GTC	TTT	CGT	GGA	AAT	GTT	GAT	AAC	AAC	ACA	CCA	TAT	GCT	AAT	1467
Glu	Met	Val	Phe	Arg	Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	
		270					275					280				
TCT	TTC	ACA	CCC	CCA	ATC	AAA	GCT	CAG	TAT	GTA	AGA	CTC	TAC	CCC	CAA	1515
Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	
	285					290					295					
ATT	TGT	CGA	AGG	CAT	TGT	ACT	TTA	AGA	ATG	GAA	CTT	CTT	GGC	TGT	GAG	1563
Ile	Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	
300					305					310					315	
CTC	TCA	GGC	TGT	TCA	GAA	CCT	TTG	GGG	ATG	AAA	TCA	GGG	CAT	ATA	CAA	1611
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	
				320					325					330		
GAC	TAC	CAG	ATC	ACT	GCC	TCC	AGC	GTC	TTC	AGA	ACA	CTC	AAC	ATG	GAC	1659
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp	
			335					340					345			
ATG	TTT	ACT	TGG	GAA	CCA	AGG	AAA	GCC	AGG	CTG	GAC	AAG	CAA	GGC	AAA	1707
Met	Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	
		350					355					360				
GTA	AAT	GCC	TGG	ACT	TCC	GGC	CAT	AAC	GAC	CAG	TCA	CAA	TGG	TTA	CAG	1755
Val	Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	
	365					370					375					

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA	1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly	
380 385 390 395	
GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT	1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala	
400 405 410	
TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG	1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln	
415 420 425	
AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG	1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg	
430 435 440	
AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT	1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu	
445 450 455	
CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC	2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly	
460 465 470 475	
TGC GCA GAG GAG GAA TGAAGTGC GGCCGCACAT CCCACAATGC TTTTCTTTAT	2098
Cys Ala Glu Glu Glu	
480	
TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAAACT GCATTTGTTT	2158
TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG	2218
CCTTTTAAAT AATTTAATTT GGTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT	2278
CTGTGAGTTA CTCTTCTTGT TCTCT	2303

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30
Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45
Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60
Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95
 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110
 Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
 115 120 125
 Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140
 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160
 His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175
 Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190
 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 195 200 205
 Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
 210 215 220
 Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
 225 230 235 240
 Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
 245 250 255
 Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
 260 265 270
 Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
 275 280 285
 Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
 290 295 300
 Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
 305 310 315 320
 Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
 325 330 335
 Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
 340 345 350
 Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
 355 360 365
 Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
 370 375 380
 Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
 385 390 395 400
 His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
 405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430
Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445
Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460
Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG	48
Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys	
1 5 10 15	
CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT	96
Arg * Gly Lys Arg Thr Ser Ser * Ile Leu * * Gly Arg Ser	
20 25 30	
CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG	144
Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr	
35 40 45	
ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC	192
Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg	
50 55 60	
TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG	240
Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln	
65 70 75 80	
TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT	288
Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly	
85 90 95	
ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA	336
Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro	
100 105 110	
GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA	384
Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser	
115 120 125	

GAT GAA GAA GAA CCA ACT TCA GCA GGT CCC TGC ACT CCT AAT CCA TGC Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro Asn Pro Cys 130 135 140	432
CAT AAT GGA GGA ACC TGT GAA ATA ACT GAA GCA TAC CGA GGG GAT ACA His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg Gly Asp Thr 145 150 155 160	480
TTC ATA GGC TAT GTT TGT AAA TGT CCC CGA GGA TTT AAT GGG ATT CAC Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn Gly Ile His 165 170 175	528
TGT CAG CAC AAC ATA AAT GAA TGC GAA GTT GAG CCT TGC AAA AAT GGT Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys Lys Asn Gly 180 185 190	576
GGA ATA TGT ACA GAT CTT GTT GCT AAC TAT TCC TGT GAG TGC CCA GGC Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu Cys Pro Gly 195 200 205	624
GAA TTT ATG GGA AGA AAT TGT CAA TAC AAA TGC TCA GGC CCA CTG GGA Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly Pro Leu Gly 210 215 220	672
ATT GAA GGT GGA ATT ATA TCA AAC CAG CAA ATC ACA GCT TCC TCT ACT Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala Ser Ser Thr 225 230 235 240	720
CAC CGA GCT CTT TTT GGA CTC CAA AAA TGG TAT CCC TAC TAT GCA CGT His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr Tyr Ala Arg 245 250 255	768
CTT AAT AAG AAG GGG CTT ATA AAT GCG TGG ACA GCT GCA GAA AAT GAC Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala Glu Asn Asp 260 265 270	816
AGA TGG AAG CGG TGG ATT CAG ATA AAT TTG CAA AGA AAA ATG AGA GTT Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys Met Arg Val 275 280 285	864
ACT GGT GTG ATT ACC CAA GGG GCC AAG AGG ATT GGA AGC CCA GAG TAT Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro Glu Tyr 290 295 300	912
ATA AAA TTC TAC AAA ATT GCC TAC AGT AAT GAT GGA AAG ACT TGG GCA Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr Trp Ala 305 310 315 320	960
ATG TAC AAA GTG AAA GGC ACC AAT GAA GAC ATG GTG TTT CGT GGA AAC Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg Gly Asn 325 330 335	1008
ATT GAT AAC AAC ACT CCA TAT GCT AAC TCT TTC ACA CCC CCC ATA AAA Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro Ile Lys 340 345 350	1056
GCT CAG TAT GTA AGA CTC TAT CCC CAA GTT TGT CGA AGA CAT TGC ACT Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His Cys Thr 355 360 365	1104
TTG CGA ATG GAA CTT CTT GGC TGT GAA CTG TCG GGT TGT TCT GAG CCT Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser Glu Pro 370 375 380	1152

CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG ATC ACT GCC TCC	1200
Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser	
385 390 395 400	
AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA CCA AGG	1248
Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg	
405 410 415	
AAA GCT CGG CTG GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC	1296
Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly	
420 425 430	
CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC	1344
His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr	
435 440 445	
AAA GTG ACT GGC ATC ATT ACA CAA GGA GCT AAA GAT TTT GGT CAT GTA	1392
Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val	
450 455 460	
CAG TTT GTT GGC TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC	1440
Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His	
465 470 475 480	
TGG ACT GTA TAC CAG GAT GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG	1488
Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln	
485 490 495	
GGA AAT TTT GAC AAT GAC ACT CAC AGA AAA AAT GTC ATC GAC CCT CCC	1536
Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro	
500 505 510	
ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT TGG TCC TGG TAC GGG AGG	1584
Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg	
515 520 525	
ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG GAG GAA TGA GGG	1632
Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu * Gly	
530 535 540	
GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT ATC TCC	1680
Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser	
545 550 555 560	
ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT	1728
Met Glu * Thr Val * Asn Leu * Glu Thr Glu Trp Phe Phe Phe	
565 570 575	
TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT	1776
Phe Ser * Lys Ser Gly Gln Ile Met Val Gly Asn * Arg Cys Phe	
580 585 590	
TAC C	1780
Tyr	

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Lys Arg Thr Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 517 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu * * Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser
1 5 10 15

Ala Thr Leu Pro Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro
20 25 30

Gly Asp Gly Ile Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly
35 40 45

Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro
50 55 60

Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly
65 70 75 80

Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser
85 90 95

Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly
100 105 110

Pro Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser
115 120 125

Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro
130 135 140

Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu
145 150 155 160

Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn
 165 170 175
 Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr
 180 185 190
 Lys Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln
 195 200 205
 Gln Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys
 210 215 220
 Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala
 225 230 235 240
 Trp Thr Ala Ala Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn
 245 250 255
 Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
 260 265 270
 Arg Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser
 275 280 285
 Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
 290 295 300
 Asp Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn
 305 310 315 320
 Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
 325 330 335
 Val Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
 340 345 350
 Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
 355 360 365
 Asp Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp
 370 375 380
 Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
 385 390 395 400
 Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
 405 410 415
 Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
 420 425 430
 Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
 435 440 445
 Tyr Ser Asn Asp Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln
 450 455 460
 Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
 465 470 475 480
 Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu
 485 490 495

Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly
 500 505 510

Cys Thr Glu Glu
 515

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
 1 5 10 15

Ser Met Glu * Thr Val * Asn Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTATT 60
ACCCAAGGAG CAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC 120
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC 180
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA 240
GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA 300
CTTCTTGGCT GTGAGCTC 318

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1 5 10 15
Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
20 25 30
Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
35 40 45
His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
50 55 60
Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
65 70 75 80
Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu
85 90 95

Asp	Gly	Xaa	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp
			100					105					110		
Lys	Glu	Phe	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met
		115					120					125			
Phe	Asn	Pro	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser
		130				135					140				
Cys	His	Arg	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu
145					150					155					160
His	Gly	Cys	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp
			165						170					175	
Ser	Gln	Met	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala
			180					185					190		
Phe	Gly	Trp	Tyr	Pro	His	Leu	Gly	Arg	Leu	Asp	Asn	Gln	Gly	Lys	Ile
		195					200					205			
Asn	Ala	Trp	Thr	Ala	Gln	Ser	Asn	Ser	Ala	Lys	Glu	Trp	Leu	Gln	Val
		210				215					220				
Asp	Leu	Gly	Thr	Gln	Arg	Gln	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala
225					230					235					240
Arg	Asp	Phe	Gly	His	Ile	Gln	Tyr	Val	Glu	Ser	Tyr	Lys	Val	Ala	His
				245					250					255	
Ser	Asp	Asp	Gly	Val	Gln	Trp	Thr	Val	Tyr	Xaa	Xaa	Glu	Glu	Gln	Gly
			260					265					270		
Ser	Ser	Lys	Val	Phe	Gln	Gly	Asn	Leu	Asp	Asn	Asn	Ser	His	Lys	Lys
		275					280					285			
Asn	Ile	Phe	Glu	Lys	Pro	Phe	Met	Ala	Arg	Tyr	Val	Arg	Val	Leu	Pro
		290				295					300				
Val	Ser	Trp	His	Asn	Arg	Ile	Thr	Leu	Arg	Leu	Glu	Leu	Leu	Gly	Cys
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys	Ser	Gly	Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln
1				5					10					15	
Ile	Thr	Ala	Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp
			20					25					30		

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
 35 40 45
 Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
 50 55 60
 Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
 65 70 75 80
 Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
 85 90 95
 Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
 100 105 110
 Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
 115 120 125
 Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
 130 135 140
 Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160
 Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
 165 170 175
 Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
 180 185 190
 Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
 195 200 205
 Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
 210 215 220
 Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240
 Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
 245 250 255
 Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
 260 265 270
 Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
 275 280 285
 Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
 290 295 300
 Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
 305 310 315 320
 Thr

(2) INFORMATION FOR SEQ ID NO:22:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1 5 10 15
Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
20 25 30
Gly Phe Thr Asp Pro Asn Cys Ser Val Val Glu Val Ala Ser Asp
35 40 45
Glu Glu Glu Pro Thr Ser Ala Gly Pro
50 55

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15
Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
20 25 30

Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT      60
GTAGGTTTCCT TTCTCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAAGTG TTCTAGTGTT      120
GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT      180
GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT      240
GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA      300
ATATGTACAG                                     310
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 549..1211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
GAATTCCGGG AGGGAGGGTA GGGGGCGGG CCGCGGGGG CCAAAGCCAG CTAGGCTCAG      60
TCTCACACGC GCGCCGCCAC TGTTTGATA TAGTGCCTC CTGGCCTCAG GCTCGCTCCC      120
CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC      180
GTGAGCCGTA GTCAGTCTG GCCGCTTCGC CTGCGTGC GCACGGAAAT CGGGGAGCCA      240
GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCTCTGCT AGACCACTCG CAGCCCCAGC      300
CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA      360
ATCACCCCTT CTCTAGGGCC ACCACTCTT TATCGCCCTT CCCAAGATTT GAGAAGCGCT      420
GCGGGAGGAA AGACGTCTCT TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG      480
CGCGCCTCGC CTAAGTGTGC CTCCGCTACG ACCCGGAGG AGCCCAGGTC ACGTCCGTGA      540
GAAGGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGACTCAG CCTCGGGGTG      600
CCCCAGTTCG GCAAAGGTGA CATTGCAAC CCGAACCCTT GTGAAAATGG TGGCATCTGT      660
CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGT CAGAAGGCTT CGCAGGTCCG      720
AACTGCTCTA GTGTTGTGGA GGTGTCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC      780
TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA      840
```

GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG 900
 CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT 960
 GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA 1020
 TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA 1080
 TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT 1140
 AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTTCAG 1200
 GTAACAGTGG GATGAGACAA ATCCATTTCC CAAATTATCA GAATCATTAT AGAAGTAGGT 1260
 TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTTAAAATG TGATTTAGTT CAGAATTAAC 1320
 ATGGTTGGAA ACTCTAAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA 1380
 ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG 1440
 AAAAAGATCT TATCATTTCA TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA 1500
 TAAATACCTA ATTGAAAAAA GTTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTCAGAG 1560
 ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTTGTGAGA AATAGTTTCC CATGTGCAAA 1620
 TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA 1680
 TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTACTIONTACA 1740
 AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA 1800
 TAGCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAAGCAG AAATGAGATG 1860
 TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT 1920
 CTTTAAGATA GTCACATAA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG 1980
 TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAAG TTTTGAAATA 2040
 AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAATCAAC 2100
 AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG 2160
 GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG 2220
 TGCCACATTT TGTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC 2280
 ACTATAATTT GAATAAAGC CGGAATTC 2308

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Arg Ser Val Ala Val Trp Leu Val Gly Leu Ser Leu Gly
 1 5 10 15

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 355 360 365
 Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu
 370 375 380
 Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa
 385 390 395 400
 Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 405 410 415
 Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys
 420 425 430
 Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 435 440 445
 Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 450 455 460
 Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 465 470 475
 Glu
 480

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.

(ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
CELL LOCUS-1

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/659,235
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-0034-696

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864/9741
(C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
 20 25 30
 Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
 35 40 45
 Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
 50 55 60
 Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
 65 70 75 80
 Leu Pro Leu Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
 20 25 30
 Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 35 40 45
 Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
 50 55 60
 Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
 65 70 75 80
 Leu Pro Val Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
 20 25 30
 His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
 35 40 45
 Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
 50 55 60
 Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
 65 70 75 80
 Ile Pro Lys Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
 20 25 30
 Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
 35 40 45
 Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
 50 55 60
 Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1 5 10 15
Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
20 25 30
Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45
Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
50 55 60
Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65 70 75 80
Arg Pro Val Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1 5 10 15
Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
20 25 30
Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
35 40 45
Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60
Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65 70 75 80
Ile Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1 5 10 15
Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
20 25 30
Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
35 40 45
Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
50 55 60
Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65 70 75 80
His Pro Leu Thr Xaa
85

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Leu Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15
Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
20 25 30
Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
50 55 60
Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65 70 75 80
Xaa Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTC	CCGGT	TA	ACTG	AGGA	CAA	AGGG	TAA	TGC	AAG	ATG	ATATTT	GATT	TCC	ATT	CTCA	60
TTCCC	AGTGG	CCTT	GATAT	TAA	ACTG	ATT	CCTG	CCACCA	GGT	CCTT	GGG	CCAC	CCTG	TTC		120
CCTGC	GTCTC	ATATTT	CTGC	ATG	CTG	CTTT	GTTT	GTATAT	AGT	GCG	CTC	TGG	CCTC	AGG		180
CTCG	CTCCCC	TCCAG	CTCTC	GCTT	CATT	TGT	TCTC	CAAGTC	AGA	AGCCCC	GCAT	CCGCC	CGG			240
CGCAG	CAGCG	TGAG	CCGTAG	TCA	CTG	CTGG	CCG	CTTCGCC	TGC	GTG	CGCG	CAC	GGA	AATC		300
GGGG	AGCCAG	GAAC	CCAAGG	AGCC	GCCGTC	CGCC	GCTGT	GCCT	CTG	CTA	GAC	CACT	CGC			360
AGCCCC	AGCC	TCT	CTCAAGC	GCAC	CCACCT	CCG	CGCACCC	CAG	CTC	AGGC	GAAG	CTGG	AG			420
TGAG	GGTGAA	TCAC	CTTTC	TCTAG	GGCCA	CCAC	TCTTTT	ATC	GCCC	CTTC	CCA	AGATT	TG			480
AGA	AGCGCTG	CGGG	AGGAAA	GAC	GTCTCT	TGAT	CTCTGA	CAG	GGCGGGG	TTT	ACTG	CTG				540
TCCTG	CAGGC	GCGC	CTCGCC	TACT	GTG	CCCC	TCCG	TACGA	CCCC	GGACCA	GCCC	AGGTCA				600
CGTCC	GTGAG	AAGGG	ATC	ATG	AAG	CAC	TTG	GTA	GCA	GCC	TGG	CTT	TTG	GTT		651
				Met	Lys	His	Leu	Val	Ala	Ala	Trp	Leu	Leu	Val		
				1				5					10			
GGA	CTC	AGC	CTC	GGG	GTG	CCC	CAG	TTC	GGC	AAA	GGT	GAC	ATT	TGC	AAC	699
Gly	Leu	Ser	Leu	Gly	Val	Pro	Gln	Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asn	
			15					20					25			
CCG	AAC	CCC	TGT	GAA	AAT	GGT	GGC	ATC	TGT	CTG	TCA	GGA	CTG	GCT	GAT	747
Pro	Asn	Pro	Cys	Glu	Asn	Gly	Gly	Ile	Cys	Leu	Ser	Gly	Leu	Ala	Asp	
			30				35					40				
GAT	TCC	TTT	TCC	TGT	GAG	TGT	CCA	GAA	GGC	TTC	GCA	GGT	CCG	AAC	TGC	795
Asp	Ser	Phe	Ser	Cys	Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	
	45					50					55					
TCT	AGT	GTT	GTG	GAG	GTT	GCA	TCA	GAT	GAA	GAA	AAG	CCT	ACT	TCA	GCA	843
Ser	Ser	Val	Val	Glu	Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	
	60				65					70					75	
GGT	CCC	TGC	ATC	CCT	AAC	CCA	TGC	CAT	AAC	GGA	GGA	ACC	TGT	GAG	ATA	891
Gly	Pro	Cys	Ile	Pro	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	
				80					85					90		
AGC	GAA	GCC	TAT	CGA	GGA	GAC	ACA	TTC	ATA	GGC	TAT	GTT	TGT	AAA	TGT	939
Ser	Glu	Ala	Tyr	Arg	Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	
			95				100						105			
CCT	CGG	GGA	TTT	AAT	GGG	ATT	CAC	TGT	CAG	CAC	AAT	ATA	AAT	GAA	TGT	987
Pro	Arg	Gly	Phe	Asn	Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	
		110				115						120				
GAA	GCT	GAG	CCT	TGC	AGA	AAT	GGC	GGA	ATA	TGT	ACC	GAC	CTT	GTT	GCT	1035

Glu	Ala	Glu	Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala		
125						130					135						
AAC	TAC	TCT	TGT	GAA	TGC	CCA	GGA	GAA	TTT	ATG	GGA	CGA	AAT	TGT	CAA	1083	
Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	155	
140					145					150							
TAT	AAA	TGC	TCT	GGG	CAC	TTG	GGA	ATC	GAA	GGT	GGG	ATC	ATA	TCT	AAT	1131	
Tyr	Lys	Cys	Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	170	
				160					165								
CAG	CAA	ATC	ACA	GCT	TCA	TCT	AAT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAG	1179	
Gln	Gln	Ile	Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	185	
				175					180								
AAG	TGG	TAT	CCC	TAC	TAT	GCT	CGA	CTT	AAT	AAG	AAG	GGC	CTT	ATA	AAT	1227	
Lys	Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	200	
				190				195				200					
GCC	TGG	ACA	GCT	GCT	GAA	AAT	GAC	AGA	TGG	CCA	TGG	ATT	CAG	ATA	AAT	1275	
Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn	215	
						210											
TTG	CAA	AGA	AAA	ATG	AGA	GTC	ACT	GGT	GTT	ATT	ACC	CAA	GGA	GCA	AAA	1323	
Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	235	
					225					230							
AGG	ATT	GGA	AGC	CCA	GAG	TAC	ATA	AAA	TCC	TAC	AAA	ATT	GCC	TAC	AGC	1371	
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser	250	
				240					245								
AAT	GAC	GGG	AAG	ACC	TGG	GCA	ATG	TAC	AAA	GTA	AAA	GGC	ACC	AAT	GAA	1419	
Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	265	
				255				260					265				
GAG	ATG	GTC	TTT	CGT	GGA	AAT	GTT	GAT	AAC	AAC	ACA	CCA	TAT	GCT	AAT	1467	
Glu	Met	Val	Phe	Arg	Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	280	
				270			275										
TCT	TTC	ACA	CCC	CCA	ATC	AAA	GCT	CAG	TAT	GTA	AGA	CTC	TAC	CCC	CAA	1515	
Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	295	
						290											
ATT	TGT	CGA	AGG	CAT	TGT	ACT	TTA	AGA	ATG	GAA	CTT	CTT	GGC	TGT	GAG	1563	
Ile	Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	315	
					305					310							
CTC	TCA	GGC	TGT	TCA	GAA	CCT	TTG	GGG	ATG	AAA	TCA	GGG	CAT	ATA	CAA	1611	
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	330	
				320					325								
GAC	TAC	CAG	ATC	ACT	GCC	TCC	AGC	GTC	TTC	AGA	ACA	CTC	AAC	ATG	GAC	1659	
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp	345	
				335				340					345				
ATG	TTT	ACT	TGG	GAA	CCA	AGG	AAA	GCC	AGG	CTG	GAC	AAG	CAA	GGC	AAA	1707	
Met	Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	360	
				350			355										
GTA	AAT	GCC	TGG	ACT	TCC	GGC	CAT	AAC	GAC	CAG	TCA	CAA	TGG	TTA	CAG	1755	
Val	Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	375	
						370					375						

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA	1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly	
380 385 390 395	
GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT	1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala	
400 405 410	
TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG	1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln	
415 420 425	
AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG	1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg	
430 435 440	
AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT	1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu	
445 450 455	
CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC	2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly	
460 465 470 475	
TGC GCA GAG GAG GAA TGAAGTGC GGCCGCACAT CCCACAATGC TTTTCTTTAT	2098
Cys Ala Glu Glu Glu	
480	
TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAAACT GCATTGTGTTT	2158
TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG	2218
CCTTTTTTAAT AATTTAATTT GGTTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT	2278
CTGTGAGTTA CTCTTCTTGT TCTCT	2303

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30
Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45
Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60
Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95
 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110
 Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
 115 120 125
 Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140
 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160
 His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175
 Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190
 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 195 200 205
 Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
 210 215 220
 Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
 225 230 235 240
 Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
 245 250 255
 Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
 260 265 270
 Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
 275 280 285
 Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
 290 295 300
 Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
 305 310 315 320
 Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
 325 330 335
 Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
 340 345 350
 Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
 355 360 365
 Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
 370 375 380
 Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
 385 390 395 400
 His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
 405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG	48
Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys	
1 5 10 15	
CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT	96
Arg * Gly Lys Arg Thr Ser Ser * Ile Leu * * Gly Arg Ser	
20 25 30	
CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG	144
Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr	
35 40 45	
ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC	192
Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg	
50 55 60	
TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG	240
Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln	
65 70 75 80	
TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT	288
Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly	
85 90 95	
ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA	336
Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro	
100 105 110	
GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA	384
Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser	
115 120 125	

GAT Asp	GAA Glu	GAA Glu	GAA Glu	CCA Pro	ACT Thr	TCA Ser	GCA Ala	GGT Gly	CCC Pro	TGC Cys	ACT Thr	CCT Pro	AAT Asn	CCA Pro	TGC Cys	432
130						135					140					
CAT His	AAT Asn	GGA Gly	GGA Gly	ACC Thr	TGT Cys	GAA Glu	ATA Ile	AGT Ser	GAA Glu	GCA Ala	TAC Tyr	CGA Arg	GGG Gly	GAT Asp	ACA Thr	480
145					150					155					160	
TTC Phe	ATA Ile	GGC Gly	TAT Tyr	GTT Val	TGT Cys	AAA Lys	TGT Cys	CCC Pro	CGA Arg	GGA Gly	TTT Phe	AAT Asn	GGG Gly	ATT Ile	CAC His	528
				165					170					175		
TGT Cys	CAG Gln	CAC His	AAC Asn	ATA Ile	AAT Asn	GAA Glu	TGC Cys	GAA Glu	GTT Val	GAG Glu	CCT Pro	TGC Cys	AAA Lys	AAT Asn	GGT Gly	576
			180					185					190			
GGA Gly	ATA Ile	TGT Cys	ACA Thr	GAT Asp	CTT Leu	GTT Val	GCT Ala	AAC Asn	TAT Tyr	TCC Ser	TGT Cys	GAG Glu	TGC Cys	CCA Pro	GGC Gly	624
		195					200					205				
GAA Glu	TTT Phe	ATG Met	GGA Gly	AGA Arg	AAT Asn	TGT Cys	CAA Gln	TAC Tyr	AAA Lys	TGC Cys	TCA Ser	GGC Gly	CCA Pro	CTG Leu	GGA Gly	672
	210					215					220					
ATT Ile	GAA Glu	GGT Gly	GGA Gly	ATT Ile	ATA Ile	TCA Ser	AAC Asn	CAG Gln	CAA Gln	ATC Ile	ACA Thr	GCT Ala	TCC Ser	TCT Ser	ACT Thr	720
225					230					235					240	
CAC His	CGA Arg	GCT Ala	CTT Leu	TTT Phe	GGA Gly	CTC Leu	CAA Gln	AAA Lys	TGG Trp	TAT Tyr	CCC Pro	TAC Tyr	TAT Tyr	GCA Ala	CGT Arg	768
				245					250					255		
CTT Leu	AAT Asn	AAG Lys	AAG Lys	GGG Gly	CTT Leu	ATA Ile	AAT Asn	GCG Ala	TGG Trp	ACA Thr	GCT Ala	GCA Ala	GAA Glu	AAT Asn	GAC Asp	816
			260					265					270			
AGA Arg	TGG Trp	AAG Lys	CGG Arg	TGG Trp	ATT Ile	CAG Gln	ATA Ile	AAT Asn	TTG Leu	CAA Gln	AGA Arg	AAA Lys	ATG Met	AGA Arg	GTT Val	864
		275					280					285				
ACT Thr	GGT Gly	GTG Val	ATT Ile	ACC Thr	CAA Gln	GGG Gly	GCC Ala	AAG Lys	AGG Arg	ATT Ile	GGA Gly	AGC Ser	CCA Pro	GAG Glu	TAT Tyr	912
	290					295					300					
ATA Ile	AAA Lys	TTC Phe	TAC Tyr	AAA Lys	ATT Ile	GCC Ala	TAC Tyr	AGT Ser	AAT Asn	GAT Asp	GGA Gly	AAG Lys	ACT Thr	TGG Trp	GCA Ala	960
305					310					315					320	
ATG Met	TAC Tyr	AAA Lys	GTG Val	AAA Lys	GGC Gly	ACC Thr	AAT Asn	GAA Glu	GAC Asp	ATG Met	GTG Val	TTT Phe	CGT Arg	GGA Gly	AAC Asn	1008
				325					330					335		
ATT Ile	GAT Asp	AAC Asn	AAC Asn	ACT Thr	CCA Pro	TAT Tyr	GCT Ala	AAC Asn	TCT Ser	TTC Phe	ACA Thr	CCC Pro	CCC Pro	ATA Ile	AAA Lys	1056
				340				345					350			
GCT Ala	CAG Gln	TAT Tyr	GTA Val	AGA Arg	CTC Leu	TAT Tyr	CCC Pro	CAA Gln	GTT Val	TGT Cys	CGA Arg	AGA Arg	CAT His	TGC Cys	ACT Thr	1104
		355					360					365				
TTG Leu	CGA Arg	ATG Met	GAA Glu	CTT Leu	CTT Leu	GGC Gly	TGT Cys	GAA Glu	CTG Leu	TCG Ser	GGT Gly	TGT Cys	TCT Ser	GAG Glu	CCT Pro	1152
	370					375					380					

CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG ATC ACT GCC TCC	1200
Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser	
385 390 395 400	
AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA CCA AGG	1248
Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg	
405 410 415	
AAA GCT CGG CTG GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC	1296
Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly	
420 425 430	
CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC	1344
His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr	
435 440 445	
AAA GTG ACT GGC ATC ATT ACA CAA GGA GCT AAA GAT TTT GGT CAT GTA	1392
Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val	
450 455 460	
CAG TTT GTT GGC TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC	1440
Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His	
465 470 475 480	
TGG ACT GTA TAC CAG GAT GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG	1488
Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln	
485 490 495	
GGA AAT TTT GAC AAT GAC ACT CAC AGA AAA AAT GTC ATC GAC CCT CCC	1536
Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro	
500 505 510	
ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT TGG TCC TGG TAC GGG AGG	1584
Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg	
515 520 525	
ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG GAG GAA TGA GGG	1632
Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu * Gly	
530 535 540	
GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT ATC TCC	1680
Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser	
545 550 555 560	
ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT	1728
Met Glu * Thr Val * Asn Leu * Glu Thr Glu Trp Phe Phe Phe	
565 570 575	
TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT	1776
Phe Ser * Lys Ser Gly Gln Ile Met Val Gly Asn * Arg Cys Phe	
580 585 590	
TAC C	1780
Tyr	

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys Arg
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Lys Arg Thr Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro
1 5 10 15

Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile
20 25 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
35 40 45

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
50 55 60

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
65 70 75 80

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
85 90 95

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
100 105 110

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
115 120 125

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
130 135 140

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
 145 150 155 160
 Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 165 170 175
 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 180 185 190
 Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 195 200 205
 Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 210 215 220
 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 225 230 235 240
 Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
 245 250 255
 Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
 260 265 270
 Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
 275 280 285
 Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
 290 295 300
 Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
 305 310 315 320
 Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
 325 330 335
 His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
 340 345 350
 Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
 355 360 365
 Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
 370 375 380
 Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 385 390 395 400
 Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu
 405 410 415
 Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe
 420 425 430
 Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 435 440 445
 Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
 450 455 460
 Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 465 470 475 480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 500 505 510

Glu

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
 1 5 10 15

Ser Met Glu

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTATT	60
ACCCAAGGAG CAAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC	120
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAG GCACCAATGA AGAGATGGTC	180
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCAATCAAA	240
GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA	300
CTTCTTGGCT GTGAGCTC	318

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln	
1 5 10 15	
Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp	
20 25 30	
Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp	
35 40 45	
His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu	
50 55 60	
Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg	
65 70 75 80	
Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu	

[illegible]

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
 1 5 10 15
 Val Pro Gln Phe Gly Lys Gly Asp Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
 1 5 10 15
 Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
 20 25 30
 Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
 35 40 45
 Glu Glu Glu Pro Thr Ser Ala Gly Pro
 50 55

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
 1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
20 25 30

Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT 60
GTAGGTTTCCT TTTCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAAC TGCTAGTGTT 120
GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT 180
GAAGCATACC GAGGGGATAC ATTATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT 240
GGGATTCAC TGCAGCACA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA 300
ATATGTACAG 310

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 550...1212
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGGC CCAAAGCCAG CTAGGCTCAG 60
TCTCACACGC GCGCCGCCAC TGTTTGTATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC 120
CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC 180
GTGAGCCGTA GTCAC TGCTG GCGCTTCGC CTGCGTGCGC GCACGGAAT CGGGGAGCCA 240
GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCTCTGCT AGACCACTCG CAGCCCCAGC 300
CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA 360
ATCACCTTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCAAGATTT GAGAAGCGCT 420
GCGGGAGGAA AGACGTCTC TTGATCTCTG ACAGGGCGGG GTTACTGCT GTCCTGCAGG 480
CGCGCTCGC CTACTGTGCC CTCCGCTACG ACCCCGGACC AGCCAGGTC ACGTCCGTGA 540
GAAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT GGA CTC AGC 591
Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
1 5 10
CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC CCG AAC CCC 639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15 20 25 30

TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT GAT TCC TTT	687
Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe	
35 40 45	
TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC TCT AGT GTT	735
Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val	
50 55 60	
GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA GGT CCC TGC	783
Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys	
65 70 75	
ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA AGC GAA GCC	831
Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala	
80 85 90	
TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT CCT CGG GGA	879
Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly	
95 100 105 110	
TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT GAA GCT GAG	927
Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu	
115 120 125	
CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT AAC TAC TCT	975
Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser	
130 135 140	
TGT GAA TGC CCA GGA GAA TTT ATG GGA CGA AAT TGT CAA TAT AAA TGC	1023
Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys	
145 150 155	
TCT GGG CAC TTG GGA ATC GAA GGT GGG ATC ATA TCT AAT CAG CAA ATC	1071
Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile	
160 165 170	
ACA GCT TCA TCT AAT CAC CGA GCT CTT TTT GGA CTC CAG AAG TGG TAT	1119
Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr	
175 180 185 190	
CCC TAC TAT GCT AGA CTT AAT AAG AAG GGC CTT ATA AAT GCC TGG ACA	1167
Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr	
195 200 205	
GCT GCT GAA AAT GAC AGA TGG CCA TGG ATT CAG GTA ACA GTG GGA TGAGA	1217
Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly	
210 215 220	
CAAATCCATT TCCCAAATTA TCAGAATCAT TATAGAAGTA GGTTAGGGAG AATTGGCTGT	1277
GATTCTTTCT CATGGTTAAA ATGTGATTTA GTTCAGAATT AACATGGTTG GAAACTCTAA	1337
AAAATGTGGA AAACAGGAAC ATTCTATGTC TGAAAATCTG AAAATAGCAT CAAGATGAAA	1397
ACATTCTTTA GTCATAAATA TACTCTTTTA AGTTATAGTA GAGAAAAAGA TCTTATCATT	1457
TCATAAGTGG ACTTTTGGGA TAGCATTGGA AATGTAAATG AAATAAATAC CTAATTGAAA	1517
AAAGTTTATT CTAAAGTGTT AATATTTAGC AACAGATTCA GAGACAAGAA AGTAACAATT	1577
CAATCTGTGT ATTTTTTGTG AGAAATAGTT TCCCATGTGC AAATATAAAG TGCGCATCAT	1637
ATCATGATAA TATCCAACGT TCTGCAGAAC TCCCTTTCAT AAATGAGAGA ATTTTAATTC	1697

ATAGTGCCTT ATATCCTCAT CAGCCATCTG ACTTTACTAC AGAAGAAAAC AATGAAATGA 1757
 TGCATTAAGT GCTTTGCTAG AAGAAACATC ATAGCAAAGC TGATAGCCCA CATTCTGTGC 1817
 ANNNAAGCTT CCAGAGCACT CGAGAAAAAG CAGAAATGAG ATGTTTTATG AAAACCGAAA 1877
 AGATAATCTG ATTTCTGTGA AATATACTTT TGATCATGTG GTTCTTTAAG ATAGTCACTA 1937
 ACAAGTCATT AGTAGCAGAT ACCAAATGGG AGAAAATTTTC CAGTATACTG AGGGTCAAGG 1997
 CAGTCATGCT GAAACTACAT GAGGTCAGGA AAGTTTTGAA ATAAGGTGAT TTTGGAAGGA 2057
 TACCTTCAAC TGGCCTAGAT TTTCAAGAAA CAGTGTAATC AACAGCCAAA CATGAGAATC 2117
 TAGCTAACAG CATTTAGAAA ACCAGAACTA AGAGTGTTAC TGGGGAATTG CATTTAAATC 2177
 CAGTATGAGA GTTTGCAAAAT GCCGTATTCT TCTAAGGGGT TTGTGCCACA TTTGTGTACC 2237
 ATGGAGTCCT CTGTAAGAAC TTTATTAGAT AAATCATCTT TACACTATAA TTTGAATAAA 2297
 AGCCGGAATT C 2308

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Lys	His	Leu	Val	Ala	Ala	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly	1	5	10	15
Val	Pro	Gln	Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asn	Pro	Asn	Pro	Cys	Glu	20	25	30	
Asn	Gly	Gly	Ile	Cys	Leu	Ser	Gly	Leu	Ala	Asp	Asp	Ser	Phe	Ser	Cys	35	40	45	
Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	50	55	60	
Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Ile	Pro	65	70	75	80
Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	85	90	95	
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	100	105	110	
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	Pro	Cys	115	120	125	
Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	130	135	140	
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly				

145					150						155				160
His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala
				165					170					175	
Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr
			180					185					190		
Tyr	Ala	Ala	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala
		195					200					205			
Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Val	Thr	Val	Gly			
	210					215					220				